VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the claims

1. **(Amended)** A screening and/or quantification method of one or more transcriptional factors(s) present in a cell or cell lysate, said method comprising the steps of:

a. binding to an insoluble solid support double-stranded DNA sequence(s) at the concentration of at least 0.01 pmole/cm^2 of said solid support surface, said double-stranded DNA sequence comprising a specific sequence, said specific sequence being able to bind said one or more transcriptional factor(s)**[**,**]** and said double-stranded DNA sequence being located from the surface of the solid support by a spacer corresponding to or comprising at least a double-stranded DNA nucleotide of at least 20 base pairs;

b. putting into contact said one or more transcriptional factor(s) with said bound double-stranded DNA sequences(s)**[**,**]**; and

c. identifying and/or quantifying a signal resulting from the binding of said transcriptional factor(s) upon said double-stranded DNA sequence(s).

3. **(Amended)** The method according to claim 1, wherein the specific sequence of the double-stranded DNA sequence(s) able to bind with the transcriptional factor(s) is located at a distance of at least about 6**[**,**]**.8 nm from the surface of the solid support.

5. **(Amended)** The method according to claim 1, wherein the signal resulting from the binding of the transcriptional factor upon the double-stranded DNA sequence is obtained through an enzymatic reaction.

6. **(Amended)** The method according to **[any of the preceding]**claim**[s]** 1 **[to 3]**, for the **[(possibly simultaneous)]** screening and/or quantification of multiple different transcriptional factors present in a same biological sample.

7. **(Amended)** The method according to claim 1, for the screening and/or quantification of transcriptional factors selected from the group consisting of NF-KB, AP-1, CREB, SP-1, C/EBP, GR, HIF-1, Myc, NF-AT, Oct, TBP, **[and]** CBF-1 and**[or]** factors listed in table 1.

8. **(Amended)** The method according to claim 1, for the screening and/or quantification of multiple different transcriptional factors upon a same support **[preferably]**upon the same multiwell plate.

10. **(Amended)** The method according to claim 1, wherein the **[double-stranded DNA sequence(s) comprise(s), between the specific sequence able to bind the transcriptional factor(s) and the solid support, a]**spacer between the double-stranded DNA sequence(s) and the solid support is**[of]**at least about 13.5 nm.

12. **(Amended)** The method according to claim 1, wherein the binding of the double-stranded DNA sequence(s) to the insoluble solid support is of non-covalent type and includes a binding pair comprising a first member and a second member, said first member being**[are]** bound to **[a first member of a binding pair able to interact with a]**the double-stranded DNA sequence, said second member**[of said binding pair]** being bound to the surface of the solid support.

34. **(Amended)** The method of Claim **[12]**36, wherein said **[first member of a]**binding pair is biotin/streptavidin.

New claims 36-38 have been added.